Amendments to the Claims

The listing of claims will replace all prior versions and listings of all claims in the application:

Claims 1-27 (cancelled)

28. (Previously presented) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

(A) receiving a protein structure of a desired target protein, said protein structure comprising:

i) a protein template structure comprising a protein backbone structure and at least one non-variable residue; and

ii) a plurality of variable residue positions;

(B) establishing a group of potential amino acid side chains for a plurality of said variable residue positions of said protein; and

(C) analyzing the interaction of all or part of each of said potential amino acid side chains from said group with all or part of the remainder of said protein structure to generate a set of optimized proteins sequences, wherein said analyzing step includes a Dead-End Elimination (DEE) computation.

29. (Previously presented) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

(A) receiving a protein structure of a desired target protein, said protein structure comprising:;

i) a protein template structure comprising a protein backbone structure and at least one non-variable residue; and

ii) a plurality of variable residue positions;

(B) classifying each variable residue position as either a core, surface or boundary residue;

(C) establishing a group of potential amino acid side chains for a plurality of said variable residue positions of said protein; and

(D) analyzing the interaction of all or part of each of said potential amino acid side chains from said group with all or part of the remainder of said protein structure to generate a set of optimized proteins sequences.

Claims 30-51 (cancelled)

52. (Previously presented) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

(A) receiving a protein structure of a desired target protein, said protein structure comprising:

i) a protein template structure comprising a protein backbone structure and at least one non-variable residue; and

ii) a plurality of variable residue positions;

(B) establishing a group of potential amino acid side chains for each of said variable residue positions, wherein the group of potential amino acids side chains for at least one of said variable residue position has an amino acid side chains selected from each of at least two different amino acid side chains; and

(C) analyzing the interaction of all or part of each of said potential amino acid side chains from said group with all or part of the remainder of said protein structure to generate a set of optimized proteins sequences.

53. (Previously presented) A method according to claim 29 or 52 wherein said analyzing step comprises a DEE computation.

54. (Previously presented) A method according to claim 28, 29, or 52 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.

55. (Currently Amended) A method according to claim ~~28 or~~ 53 wherein said DEE computation is selected from the group consisting of original DEE and Goldstein DEE.

56. (Currently Amended) A method according to claim ~~28 or~~ 53 wherein said analyzing step includes the use of at least one scoring function.

57. (Previously presented) A method according to claim 56 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

58. (Previously presented) A method according to claim 57 wherein said analyzing step includes the use of at least two scoring functions.

59. (Previously presented) A method according to claim 57 wherein said analyzing step includes the use of at least three scoring functions.

60. (Previously presented) A method according to claim 57 wherein said analyzing step includes the use of at least four scoring functions.

61. (Previously presented) A method according to claim 57 wherein said scoring function is an atomic solvation scoring function.

62. (Previously presented) A method according to claim 57 wherein said atomic solvation scoring function includes a scaling factor that compensates for over-counting.

63. (Previously presented) A method according to claim 28, 29, or 52 further comprising experimentally testing at least one member of said set.

64. (Previously presented) A method according to claim 54 further comprising the step of: generating a list of additional optimal sequences from said globally optimal protein sequence.

65. (Previously presented) A method according to claim 63 wherein said generating includes the use of a Monte Carlo search.

66. (Previously presented) A method according to claim 28, 29, or 52 wherein said analyzing step comprises a Monte Carlo computation.

67. (Currently Amended) A method according to claim 63 further comprising the step of: testing some or all of said protein sequences from said ~~list~~ set to produce potential energy test results.

68. (Previously presented) A method according to claim 67 further comprising the step of: analyzing the correspondence between said potential energy test results and theoretical potential energy data.

69. (Previously presented) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

(A) receiving a protein structure of a desired target protein, said protein structure comprising:

i) a protein template structure comprising a protein backbone structure and at least one non-variable residue; and

ii) a plurality of variable residue positions;

(B) establishing a group of potential amino acid side chains for a plurality of variable residue positions of said protein, wherein at least one of said amino acid side chains is from a hydrophilic amino acid; and

(C) analyzing the interaction of all or part of each of said potential amino acid side chains from said group with all or part of said protein structure to generate a set of optimized proteins sequences, wherein said analyzing step includes the use of at least one scoring function.

Claim 70 (cancelled)

71. (Currently amended) A method according to claim 28, 29, 52, or [[71]]69 further comprising modulating the protein backbone structure.

72. (Previously presented) A method according to claim 28, 29, 52, or 71 wherein said variable residue positions comprise one or more non-core positions.

73. (Previously presented) A method according to claim 28, 29, 52, or 69 wherein at least one scoring function is used at a first variable position and at least one scoring function is used at a second variable position, wherein said scoring functions are different.

74. (Currently amended) A method according to 28, 29, 52, or 69 wherein step (c) comprises a second group for a second variable position which has a second set of at least two amino acid side chains,

75. (Currently amended) A method according to [[76]] claim 74 wherein said first and second amino acid side chains are different.

76. (Currently amended) A method according to [[76]] claim 74 wherein said first and second amino acid side chains are the same.

77. (Previously presented) A method according to 28, 29, 52, or 69 wherein said non-variable residues are fixed.

78. (Previously presented) A method according to 28, 29, 52, or 69 wherein said non-variable residues are floated.

79. (Previously presented) A method according to claim 28, 29, 52, or 69 wherein said variable residue positions are structurally functional residue positions.

80. (Previously presented) A method according to claim 28, 29, 52, or 69 wherein said variable residue positions are biologically functional residue positions.

81. (New) A method according to claim 28 wherein said DEE computation is selected from the group consisting of original DEE and Goldstein DEE.

82. (New) A method according to claim 28 wherein said analyzing step includes the use of at least one scoring function.

83. (New) A method according to claim 82 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

84. (New) A method according to claim 83 wherein said analyzing step includes the use of at least two scoring functions.

85. (New) A method according to claim 83 wherein said analyzing step includes the use of at least three scoring functions.

86. (New) A method according to claim 83 wherein said analyzing step includes the use of at least four scoring functions.

87. (New) A method according to claim 83 wherein said scoring function is an atomic solvation scoring function.

88. (New) A method according to claim 83 wherein said atomic solvation scoring function includes a scaling factor that compensates for over-counting.

89. (New) A method according to claim 28, 29, 52 and 69 wherein at least one potential amino acid side chain is hydrophilic.

90. (New) A method according to claim 89 wherein said potential amino acid side chain is selected from the group consisting of serine, threonine, aspartic acid, asparagine, glutamine, glutamic acid, arginine, lysine, and histidine.